

What is claimed is:

1. A method for analyzing proteins according to which two types of samples containing proteins are compared using a mass spectrometer, so that the proteins which are included in respective samples are identified and the mass ratio of a protein of the same type that is included in the respective samples is analyzed, wherein the method for analyzing proteins is characterized by including the steps of:

respectively digesting said two types of samples containing proteins at portions of a certain amino acid using a restriction enzyme so as to prepare samples containing peptides;

modifying peptides which are included in said respective samples containing peptides with labeling compounds having different masses due to isotopes, so that peptides of the same type that are included in the respective samples containing peptides have different masses;

mixing the samples containing peptides that have been respectively labeled with isotopes, separating and quantifying the mixed sample for each peptide and measuring the MS spectrum, and finding the content ratio of peptides of the same type having different masses due to isotope labeling;

selecting a peptide of which the amino acid sequence should be identified from among the peptides in reference to said MS spectrum and qualitatively analyzing the amino acid sequence of selected peptide from the mass spectrum of the product ions which are generated from the peptide;

identifying a corresponding protein from known-DNA sequences on the basis of the amino acid sequence of said peptide; and

finding the ratio of the content of said identified protein included in said samples containing respective proteins on the basis of the value obtained from separation quantification using the difference in the mass of said peptides that have been modified with isotopes.

2. The method for analyzing proteins according to Claim 1, characterized in that

O-methyl-isourea and its stable isotopes are used as said labeling compounds.

3. The method for analyzing proteins according to Claim 2, characterized in that
in said step of finding the content ratio of peptides of the same type, when
two peaks of peptides of the same type having different masses due to said modifying
compounds in the MS spectrum are compared, the quantitative ratio is corrected by
getting rid of the overlapping region with the peak of a peptide labeled with an
naturally-occurring isotope.